

WEST Search History



DATE: Wednesday, September 22, 2004

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
		<i>DB=PGPB,USPT; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L5	transcriptionally silent information	0
<input type="checkbox"/>	L4	L3 and impair\$	85
<input type="checkbox"/>	L3	L2 and select\$ [clm]	223
<input type="checkbox"/>	L2	L1 and plant	303
<input type="checkbox"/>	L1	transcriptional gene silenc\$	329

END OF SEARCH HISTORY

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* * * * * Welcome to STN International * * * * *

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NEWS	9	AUG 27	BIOCOMMERCE: Changes and enhancements to content coverage
NEWS	10	AUG 27	BIOTECHABS/BIOTECHDS: Two new display fields added for legal status data from INPADOC
NEWS	11	SEP 01	INPADOC: New family current-awareness alert (SDI) available
NEWS	12	SEP 01	New pricing for the Save Answers for SciFinder Wizard within STN Express with Discover!
NEWS	13	SEP 01	New display format, HITSTR, available in WPIDS/WPINDEX/WPIX
NEWS	14	SEP 14	STN Patent Forum to be held October 13, 2004, in Iselin, NJ
NEWS EXPRESS	JULY 30 CURRENT WINDOWS VERSION IS V7.01, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 11 AUGUST 2004		
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NEWS LOGIN	Welcome Banner and News Items		
NEWS PHONE	Direct Dial and Telecommunication Network Access to STN		
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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 13:37:56 ON 22 SEP 2004

=> file agricola caplus biosis
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION

FULL ESTIMATED COST

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0.21

FILE 'AGRICOLA' ENTERED AT 13:38:03 ON 22 SEP 2004

FILE 'CAPLUS' ENTERED AT 13:38:03 ON 22 SEP 2004

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FILE 'BIOSIS' ENTERED AT 13:38:03 ON 22 SEP 2004

Copyright (c) 2004 The Thomson Corporation.

=> s transcriptional gene silenc?

L1 833 TRANSCRIPTIONAL GENE SILENC?

=> s l1 and plant?

L2 645 L1 AND PLANT?

=>

=> s l2 and (defect? or impair? or muta?)

L3 141 L2 AND (DEFECT? OR IMPAIR? OR MUTA?)

=> s l3 and select?

L4 11 L3 AND SELECT?

=> dup rem l4

PROCESSING COMPLETED FOR L4

L5 7 DUP REM L4 (4 DUPLICATES REMOVED)

=> d 1-7 ti

L5 ANSWER 1 OF 7 AGRICOLA Compiled and distributed by the National
Agricultural Library of the Department of Agriculture of the United States
of America. It contains copyrighted materials. All rights reserved.
(2004) on STN DUPLICATE 1

TI Short **defective** interfering RNAs of tombusviruses are not
targeted but trigger post-**transcriptional gene**
silencing against their helper virus.

L5 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN

TI High-oleic and high-stearic cottonseed oils: nutritionally improved
cooking oils developed using gene silencing

L5 ANSWER 3 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 2

TI Virus variation in relation to resistance-breaking in **plants**

L5 ANSWER 4 OF 7 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN

TI The abundant retinal protein of the Chlamydomonas eye is not the
photoreceptor for phototaxis and photophobic responses.

L5 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN

TI A library of Arabidopsis 35S-cDNA lines for identifying novel
mutants

L5 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN

TI **Selective** inhibition of gene expression by RNAi in chick embryos
in ovo

L5 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3

TI Cytosine methylation at CG and CNG sites is not a prerequisite for the
initiation of **transcriptional gene silencing**
in **plants**, but it is required for its maintenance

=> d 5 ab

L5 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN
AB We have developed a system to over-express or co-suppress random cDNAs in Arabidopsis thaliana upon Agrobacterium tumefaciens-mediated transformation. We constructed a binary vector containing a novel Arabidopsis cDNA library driven by the cauliflower mosaic virus (CaMV) 35S promoter. The vector, 35SpBARN, offers in terra **selection** with glufosinate ammonium (BASTA) and the ability to identify the cDNA insert using PCR with flanking primers. We introduced this overexpression library into Arabidopsis and **selected** over 30 000 transformants. A random sample of 50 T1 **plants** was analyzed to determine the quality of the cDNA library in **planta**. About 90% of T1 **plants** in the collection have inserts, the average insert size is ca. 1.1 kb, and ca. 43% of these inserts appear to encode full-length proteins. T1 **plants** were screened for visible abnormalities, and one **mutant**, V5, was chosen for further study. This **mutant** displays a pale green phenotype, and its transgene contains a partial petH cDNA encoding chloroplast ferredoxin-NADP+ reductase (EC 1.18.1.2). This construct co-suppresses the endogenous petH transcript. We recapitulated the **mutant** phenotype by expressing either the full-length or truncated petH cDNA from the CaMV 35S promoter in wild-type Arabidopsis. Our results indicate that co-suppressing endogenous genes can cause dominant phenotypes as expected. As we have also used the 35SpBARN vector to successfully over-express other transcripts in **planta**, we predict that this system will be generally useful for identifying genes that yield phenotypes upon over-expression as well.

=> d 7 ab

L5 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3
AB Transgenes integrated into **plant** chromosomes, and/or endogenous **plant** genes, may be subjected to epigenetic silencing at the transcriptional or post-transcriptional level. Transcriptional inactivation is correlated with hypermethylation of CG/CNG sites at the silent loci. It is not known whether local hyper- methylation is part of the inactivation process, or just an outcome of the silent state. To address this issue, we generated transgenic tobacco lines containing a **selectable** marker gene controlled by a derivative of the 35S promoter of the cauliflower mosaic virus (CaMV) devoid of CG and CNG methylation acceptor sites. Silencing was triggered by crossing to the silencer locus of tobacco line 271. This line contains inactive and methylated copies of the 35S promoter and is able to silence homologous promoter copies at ectopic chromosomal positions. The **mutated** promoter lacking CG/CNG methylation acceptor sites was as susceptible to Trans-silencing as the unmodified 35S promoter control. Thus, methylation at CG and CNG sites is not a prerequisite for the initiation of epigenetic gene inactivation. Interestingly, while methylation of the remaining cytosines is usually only slightly affected by silencing, it was significantly increased in the absence of CG/CNG sequences. Since this sequence preference is the same as that of known methyltransferases, this may imply that silencing is accompanied or directly followed by recruitment of methyltransferase, which, in the absence of cytosines in the optimal sequence context, modifies other C residues in the affected area. However, silencing without CG/CNG methylation was immediately relieved in the absence of the silencer. Thus, CG/CNG methylation is probably essential for the maintenance of previously established epigenetic states.

=> d 7 so

L5 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3

SO Molecular & General Genetics (1998), 259(2), 207-215
CODEN: MGGEAE; ISSN: 0026-8925

=> s l3 and epigenet?

L6 23 L3 AND EPIGENET?

=> dup rem l6

PROCESSING COMPLETED FOR L6

L7 15 DUP REM L6 (8 DUPLICATES REMOVED)

=> d 1-15 ti

- L7 ANSWER 1 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
TI BRU1, a novel link between responses to DNA damage and **epigenetic** gene silencing in Arabidopsis
- L7 ANSWER 2 OF 15 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Maintenance of CpG methylation is essential for **epigenetic** inheritance during **plant** gametogenesis.
- L7 ANSWER 3 OF 15 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
TI RNA-directed DNA methylation in Arabidopsis.
- L7 ANSWER 4 OF 15 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN DUPLICATE 2
TI Two regulatory levels of **transcriptional gene silencing** in Arabidopsis.
- L7 ANSWER 5 OF 15 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
TI HDA6, a putative histone deacetylase needed to enhance DNA methylation induced by double-stranded RNA.
- L7 ANSWER 6 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
TI ROS1, a repressor of **transcriptional gene silencing** in Arabidopsis, encodes a DNA glycosylase/lyase
- L7 ANSWER 7 OF 15 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Homology-dependent gene silencing mechanisms in fungi.
- L7 ANSWER 8 OF 15 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI A truncated form of the human CAF-1 p150 subunit **impairs** the maintenance of **transcriptional gene silencing** in mammalian cells.
- L7 ANSWER 9 OF 15 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI PTGS in **plants**, a virus resistance mechanism.
Original Title: L'inactivation **epigenetique** post-transcriptionnelle chez les vegetaux: Un mecanisme de resistance aux virus.
- L7 ANSWER 10 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3

- TI Blocking histone deacetylation in Arabidopsis induces pleiotropic effects on **plant** gene regulation and development
- L7 ANSWER 11 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 4
- TI Endogenous targets of **transcriptional gene silencing** in arabidopsis
- L7 ANSWER 12 OF 15 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
- TI **Transcriptional gene silencing mutants.**
- L7 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5
- TI Disruption of the **plant** gene MOM releases transcriptional silencing of methylated genes
- L7 ANSWER 14 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 6
- TI Gene silencing: RNA makes RNA makes no protein
- L7 ANSWER 15 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 7
- TI Cytosine methylation at CG and CNG sites is not a prerequisite for the initiation of **transcriptional gene silencing** in **plants**, but it is required for its maintenance

=> d ab

- L7 ANSWER 1 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
- AB DNA repair associated with DNA replication is important for the conservation of genomic sequence information, whereas reconstitution of chromatin after replication sustains **epigenetic** information. We have isolated and characterized **mutations** in the BRU1 gene of Arabidopsis that suggest a novel link between these underlying maintenance mechanisms. Bru1 **plants** are highly sensitive to genotoxic stress and show stochastic release of **transcriptional gene silencing**. They also show increased intrachromosomal homologous recombination and constitutively activated expression of poly (ADP-ribose) polymerase-2 (AtPARP-2), the induction of which is associated with elevated DNA damage. Bru1 **mutations** affect the stability of heterochromatin organization but do not interfere with genome-wide DNA methylation. BRU1 encodes a novel nuclear protein with two predicted protein-protein interaction domains. The developmental abnormalities characteristic of bru1 **mutant plants** resemble those triggered by **mutations** in genes encoding subunits of chromatin assembly factor (CAF-1), the condensin complex, or MRE11. Comparison of bru1 with these **mutants** indicates cooperative roles in the replication and stabilization of chromatin structure, providing a novel link between chromatin replication, **epigenetic** inheritance, S-phase DNA damage checkpoints, and the regulation of meristem development.

=> d 4 ab

- L7 ANSWER 4 OF 15 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN DUPLICATE 2
- AB In mammals, some fungi, and **plants**, DNA methylation plays a central role in the **epigenetic** control of gene transcription. Recently, however, a subclass of Arabidopsis **mutants** revealed that the release of **transcriptional gene**

silencing (TGS) does not necessarily require DNA demethylation. Here, we address the fundamental question of whether these **mutants** delineate a previously uncharacterized, methylation-independent level of **epigenetic** regulation, or whether they just act downstream of DNA methylation signals. Two **mutants** described earlier, *ddm1* and *mom1*, reactivate previously silent loci: *ddm1* **impairs** TGS by reducing chromosomal DNA methylation, and *mom1* releases TGS without affecting DNA methylation. We examined the epistatic relationship between *ddm1* and *mom1* by constructing double **mutant** strains. The synergistic release of TGS revealed by gene expression patterns from silent loci, drastic developmental abnormalities, and characteristic changes in nuclear architecture in these double **mutants** implies that DDM1 and MOM are likely to operate at independent levels in TGS control. Our results indicate that the methylation-independent silencing mechanism reinforces the methylation-based system and prevents extremely rapid **epigenetic** deregulation in **plants** with DNA methylation deficiencies.

=> d 4 so

- L7 ANSWER 4 OF 15 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved.
(2004) on STN DUPLICATE 2
- S0 Proceedings of the National Academy of Sciences of the United States of America, Oct 15, 2002. Vol. 99, No. 21. p. 13659-13662
Publisher: Washington, D.C. : National Academy of Sciences,
CODEN: PNASA6; ISSN: 0027-8424

=> d so

- L7 ANSWER 1 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
- S0 Genes & Development (2004), 18(7), 782-793
CODEN: GEDEEP; ISSN: 0890-9369

=> d 6 ab

- L7 ANSWER 6 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
- AB **Mutations** in the Arabidopsis ROS1 locus cause transcriptional silencing of a transgene and a homologous endogenous gene. In the *ros1* **mutants**, the promoter of the silenced loci is hypermethylated, which may be triggered by small RNAs produced from the transgene repeats. The transcriptional silencing in *ros1* **mutants** can be released by the *ddm1* **mutation** or the application of the DNA methylation inhibitor 5-aza-2'-deoxycytidine. ROS1 encodes an endonuclease III domain nuclear protein with bifunctional DNA glycosylase/lyase activity against methylated but not unmethylated DNA. The *ros1* **mutant** shows enhanced sensitivity to genotoxic agents Me methanesulfonate and hydrogen peroxide. We suggest that ROS1 is a DNA repair protein that represses homol.-dependent **transcriptional gene silencing** by demethylating the target promoter DNA.

=> d 11 ab

- L7 ANSWER 11 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 4
- AB **Transcriptional gene silencing** (TGS) frequently inactivates foreign genes integrated into **plant** genomes but very likely also suppresses an unknown subset of chromosomal information. Accordingly, RNA anal. of **mutants impaired** in silencing should uncover endogenous targets of this **epigenetic**

regulation. We compared transcripts from wild-type Arabidopsis carrying a silent transgene with RNA from an isogenic transgene-expressing TGS **mutant**. Two cDNA clones were identified representing endogenous RNA expressed only in the **mutant**. The synthesis of these RNAs was found to be released in several **mutants** affected in TGS, implying that TGS in general and not a particular **mutation** controls the transcriptional activity of their templates. Detailed anal. revealed that the two clones are part of longer transcripts termed TSI (for transcriptionally silent information). Two major classes of related TSI transcripts were found in a **mutant** cDNA library. They are synthesized from repeats present in heterochromatic pericentromeric regions of Arabidopsis chromosomes. These repeats share sequence homol. with the 3' terminal part of the putative retrotransposon Athila. However, the transcriptional activation does not include the transposon itself and does not promote its movement. There is no evidence for a general release of silencing from retroelements. Thus, foreign genes in **plants** encounter the **epigenetic** control normally directed, at least in part, toward a subset of pericentromeric repeats.

=> d 11 so

L7 ANSWER 11 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 4
 SO Plant Cell (2000), 12(7), 1165-1178
 CODEN: PLCEEW; ISSN: 1040-4651

=> d 12 ab

L7 ANSWER 12 OF 15 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN

=> d 12 so

L7 ANSWER 12 OF 15 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
 SO Plant molecular biology, June 2000. Vol. 43, No. 2/3. p. 235-241
 Publisher: Dordrecht : Kluwer Academic Publishers.
 CODEN: PMBIDB; ISSN: 0167-4412

=> d 13 ab

L7 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5
 AB **Epigenetic** modifications change transcription patterns in multi-cellular organisms to achieve tissue-specific gene expression and inactivate alien DNA such as transposons or transgenes. In **plants** and animals, DNA methylation is involved in heritability and flexibility of **epigenetic** states, although its function is far from clear. We have isolated an Arabidopsis gene, MOM, whose product is required for the maintenance of **transcriptional gene silencing**. **Mutation** of this gene or depletion of its transcript by expression of antisense RNA reactivates transcription from several previously silent, heavily methylated loci. Despite this, the dense methylation at these reactivated loci is maintained even after nine generations, indicating that transcriptional activity and methylation pattern are inherited independently. The predicted MOM gene product is a nuclear protein of 2,001 amino acids containing a region similar to part of the ATPase region of the SWI2/SNF2 family, members of which are involved

in chromatin remodelling. MOM is the first known mol. component that is essential for **transcriptional gene silencing** and does not affect methylation pattern. Thus, it may act downstream of methylation in **epigenetic** regulation, or be part of a new pathway that does not require methylation marks.

=> d 13 so

L7 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5
SO Nature (London) (2000), 405(6783), 203-206
CODEN: NATUAS; ISSN: 0028-0836

=> d 14 ab

L7 ANSWER 14 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 6
AB A review with 12 refs. A **mutation** that disrupts post-**transcriptional gene silencing** in *Neurospora crassa* has been found to affect the homolog of a **plant**-encoded RNA-dependent RNA polymerase. This enzyme may produce a specificity determinant of gene silencing and mediate an **epigenetic** conversion at the RNA level.

=> d 14 so

L7 ANSWER 14 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 6
SO Current Biology (1999), 9(16), R599-R601
CODEN: CUBLE2; ISSN: 0960-9822

=> s transcriptionally silenced information

L8 0 TRANSCRIPTIONALLY SILENCED INFORMATION

=> s transcriptionally silent information

L9 4 TRANSCRIPTIONALLY SILENT INFORMATION

=> dup rem l9

PROCESSING COMPLETED FOR L9

L10 2 DUP REM L9 (2 DUPLICATES REMOVED)

=> d 1-2 ti

L10 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN
TI Cloning of transcriptionally silenced plant genes

L10 ANSWER 2 OF 2 AGRICOLA Compiled and distributed by the National
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(2004) on STN DUPLICATE 1

TI Endogenous targets of transcriptional gene silencing in *Arabidopsis*.

=> d a

'A' IS NOT A VALID FORMAT

In a multifile environment, a format can only be used if it is valid in at least one of the files. Refer to file specific help messages or the STNGUIDE file for information on formats available in individual files.

REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):bab

'BAB' IS NOT A VALID FORMAT

In a multifile environment, a format can only be used if it is valid in at least one of the files. Refer to file specific help messages

or the STNGUIDE file for information on formats available in individual files.

REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):ab

L10 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN

AB The invention relates to gene silencing as observed after integration of transgenes into plant genomes. RNA anal. of mutants impaired in silencing should uncover endogenous targets of the transcriptional silencing system. Comparison of transcriptional gene expression between an Arabidopsis line carrying a silent transgene present in multiple copies and its mutant derivative mom1 impaired in silencing of the transgene revealed two cDNA clones which are expressed in the mutant plants, but not in the parental and not in wild type plants. Detailed anal. revealed that the two clones (TSI-A and TSI-B) are part of longer transcripts termed TSI (**Transcriptionally Silent Information**).

Genomic templates encoding TSI are repetitive elements with mainly pericentromeric location and conserved organization among various ecotypes. These repeats share sequence homol. with the 3'-terminal part of the putative retrotransposon Athila. However, the transcription activation does not include retrotransposon itself and does not promote its movement. Transcriptional silencing of the genomic TSI templates is specifically released in the mutant. Transcription of TSI can be used as a marker to identify a defective silencing pathway in a plant.

=> d pi

L10 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001020010	A2	20010322	WO 2000-EP8994	20000914
WO 2001020010	A3	20020117		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1212445	A2	20020612	EP 2000-967677	20000914
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL			
JP 2003509056	T2	20030311	JP 2001-523781	20000914

=> s ((steimer a?) or (steimer, a?))/au

L11 9 ((STEIMER A?) OR (STEIMER, A?))/AU

=> dup rem l11

PROCESSING COMPLETED FOR L11

L12 5 DUP REM L11 (4 DUPLICATES REMOVED)

=> d 1-5 ti

L12 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1

TI Epigenetic control of plant development: new layers of complexity

L12 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN

TI Cloning of transcriptionally silenced plant genes

L12 ANSWER 3 OF 5 AGRICOLA Compiled and distributed by the National

Agricultural Library of the Department of Agriculture of the United States

of America. It contains copyrighted materials. All rights reserved.
 (2004) on STN DUPLICATE 2

TI Apomixis in agriculture: the quest for clonal seeds.

L12 ANSWER 4 OF 5 AGRICOLA Compiled and distributed by the National
 Agricultural Library of the Department of Agriculture of the United States
 of America. It contains copyrighted materials. All rights reserved.
 (2004) on STN DUPLICATE 3

TI Endogenous targets of transcriptional gene silencing in Arabidopsis.

L12 ANSWER 5 OF 5 AGRICOLA Compiled and distributed by the National
 Agricultural Library of the Department of Agriculture of the United States
 of America. It contains copyrighted materials. All rights reserved.
 (2004) on STN

TI Epigenetic control of plant development: new layers of complexity.

=> d 5 ab

L12 ANSWER 5 OF 5 AGRICOLA Compiled and distributed by the National
 Agricultural Library of the Department of Agriculture of the United States
 of America. It contains copyrighted materials. All rights reserved.
 (2004) on STN

=> d 5 so

L12 ANSWER 5 OF 5 AGRICOLA Compiled and distributed by the National
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 (2004) on STN

SO Current opinion in plant biology, p. 11-19
 ISSN: 1369-5266

=> d so

L12 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1

SO Current Opinion in Plant Biology (2004), 7(1), 11-19
 CODEN: COBPFZ; ISSN: 1369-5266

=> s ((scheid, o?) or scheid o?)/au
 UNMATCHED RIGHT PARENTHESIS 'O?)/AU'
 The number of right parentheses in a query must be equal to the
 number of left parentheses.

=> s ((scheid, o?) or (scheid o?))/au
 L13 64 ((SCHEID, O?) OR (SCHEID O?))/AU

=> s l13 and silenc?
 L14 33 L13 AND SILENC?

=> s l14 and plant?
 L15 31 L14 AND PLANT?

=> dup rem l15
 PROCESSING COMPLETED FOR L15
 L16 17 DUP REM L15 (14 DUPLICATES REMOVED)

=> d 1-10 ti

L16 ANSWER 1 OF 17 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1

TI Arabidopsis histone deacetylase HDA6 is required for maintenance of

transcriptional gene **silencing** and determines nuclear organization of rDNA repeats

- L16 ANSWER 2 OF 17 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 2
TI BRU1, a novel link between responses to DNA damage and epigenetic gene **silencing** in Arabidopsis
- L16 ANSWER 3 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Two means of transcriptional reactivation within heterochromatin.
- L16 ANSWER 4 OF 17 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3
TI Formation of stable epialleles and their paramutation-like interaction in tetraploid Arabidopsis thaliana
- L16 ANSWER 5 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Maintenance of CpG methylation is essential for epigenetic inheritance during **plant** gametogenesis.
- L16 ANSWER 6 OF 17 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN DUPLICATE 4
TI Two regulatory levels of transcriptional gene **silencing** in Arabidopsis.
- L16 ANSWER 7 OF 17 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5
TI Endogenous targets of transcriptional gene **silencing** in arabidopsis
- L16 ANSWER 8 OF 17 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN DUPLICATE 6
TI Transcriptional gene **silencing** mutants.
- L16 ANSWER 9 OF 17 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 7
TI Disruption of the **plant** gene MOM releases transcriptional **silencing** of methylated genes
- L16 ANSWER 10 OF 17 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN DUPLICATE 8
TI Release of epigenetic gene **silencing** by trans-acting mutations in Arabidopsis.

=> d 10 ab

- L16 ANSWER 10 OF 17 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN DUPLICATE 8
- AB Gene **silencing** in **plants** inactivates transgenes introduced into **plants** and/or endogenous homologous genes. This stable but potentially reversible loss of gene activity resembles epigenetic changes that occur in normal development. The stability of **silencing** implies the involvement of trans-acting components, although none of them have been identified so far. Here we report the finding of second-site mutations interfering with maintenance of the silent state. We mutagenized Arabidopsis thaliana **plants** carrying a silent transgene encoding hygromycin phosphotransferase (hpt)

and therefore show a heritable hygromycin-sensitive phenotype. The M2 generation was screened for hygromycin resistance. Eight putative mutants (som1 to 8) were found that expressed the transgene and transmitted the expressed state to their progeny. All mutations were shown to reactivate a silent transgenic test locus in trans. The level of DNA methylation at the hpt locus and at centromeric repeats was found to be reduced in the som mutants. Complementation crosses indicated complex epigenetic interactions among the som mutant alleles and with the previously described ddm1 allele, which elicits DNA hypomethylation [Vongs, A., Kakutani, T., Martienssen, R.A. & Richards, E.J. (1993) Science 260, 1926-1928]. Som mutants can be classified into three groups: (i) allelic or interacting with ddm1 and with each other (som 1, 4, and 5), (ii) nonallelic with ddm1 and som mutants of group A (som2), and (iii) mutants with slow resilencing after outcrosses, which hinders their classification (som 3, 6, 7, and 8).

=> d 11-17 ti

- L16 ANSWER 11 OF 17 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 9
TI Cytosine methylation at CG and CNG sites is not a prerequisite for the initiation of transcriptional gene **silencing in plants**, but it is required for its maintenance
- L16 ANSWER 12 OF 17 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 10
TI Methylation of cytosines in nonconventional methylation acceptor sites can contribute to reduced gene expression
- L16 ANSWER 13 OF 17 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN DUPLICATE 11
TI A change of ploidy can modify epigenetic **silencing**.
- L16 ANSWER 14 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Epigenetic gene **silencing** in Arabidopsis: Genetic triggers and molecular consequences.
- L16 ANSWER 15 OF 17 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
TI Gene inactivation in Arabidopsis thaliana is not accompanied by an accumulation of repeat-induced point mutations.
- L16 ANSWER 16 OF 17 CAPLUS COPYRIGHT 2004 ACS on STN
TI Inactivation of repeated genes - DNA-DNA interaction?
- L16 ANSWER 17 OF 17 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
TI Two means of transcriptional reactivation within heterochromatin.

=> d 14 ab

- L16 ANSWER 14 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN

=> d 14 so

- L16 ANSWER 14 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on

STN
SO Journal of Applied Genetics, (1996) Vol. 37A, No. 0, pp. 52-53.
Meeting Info.: International Conference on Perspectives in Plant Genetics.
Warsaw, Poland. September 16-17, 1996.
ISSN: 1234-1983.

=> s ((paszkowski j?) or (paszkowski, j?))/au
L17 254 ((PASZKOWSKI J?) OR (PASZKOWSKI, J?))/AU

=> s l17 and silenc?
L18 52 L17 AND SILENC?

=> s l18 and plant?
L19 50 L18 AND PLANT?

=> s l19 and transcript?
L20 33 L19 AND TRANSCRIPT?

=> dup rem l20
PROCESSING COMPLETED FOR L20
L21 19 DUP REM L20 (14 DUPLICATES REMOVED)

=> d 1-10 ti

L21 ANSWER 1 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
TI BRU1, a novel link between responses to DNA damage and epigenetic gene
silencing in Arabidopsis

L21 ANSWER 2 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN
TI DNA and histone methylation in **plants**

L21 ANSWER 3 OF 19 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
TI Two means of **transcriptional** reactivation within
heterochromatin.

L21 ANSWER 4 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN
TI Formation of stable epialleles and their paramutation-like interaction in
tetraploid Arabidopsis thaliana

L21 ANSWER 5 OF 19 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
TI Maintenance of CpG methylation is essential for epigenetic inheritance
during **plant** gametogenesis.

L21 ANSWER 6 OF 19 AGRICOLA Compiled and distributed by the National
Agricultural Library of the Department of Agriculture of the United States
of America. It contains copyrighted materials. All rights reserved.
(2004) on STN DUPLICATE 2
TI Two regulatory levels of **transcriptional** gene **silencing**
in Arabidopsis.

L21 ANSWER 7 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3
TI Depletion of MOM1 in non-dividing cells of Arabidopsis **plants**
releases **transcriptional** gene **silencing**

L21 ANSWER 8 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN
TI Cloning of **transcriptionally silenced plant**
genes

L21 ANSWER 9 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN
TI Gene involved in epigenetic gene **silencing**

L21 ANSWER 10 OF 19 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
TI Epigenetic developmental mechanisms in **plants**: Molecules and
targets of **plant** epigenetic regulation.

=> d 7 ab

L21 ANSWER 7 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3
AB Mitotic and meiotic inheritance of epigenetic information is coupled to
the reproduction of chromatin conformation and DNA methylation patterns. This
implies that the S phase of the cell cycle provides a window of
opportunity for changes in epigenetic determination Recent studies, however,
have suggested that chromatin structure is also rather dynamic in quiescent
cells of multicellular eukaryotes and that silent heterochromatic regions
can become accessible to **transcription**. Such epigenetic
flexibility in differentiated tissues could be of physiol. importance.
The mechanisms and mol. components involved are of great interest but as
yet unknown. We examined MOM1 (Morpheus' Mol. 1), a regulator of
transcriptional gene silencing (TGS) that acts
independently of DNA methylation, for its role in the maintenance of TGS
in non-dividing, differentiated cells. The results provide evidence that
TGS maintenance mediated by MOM1 is a dynamic process that can be modified
in non-dividing cells of mature **plant** organs by depletion of
MOM1.

=> d 7 so

L21 ANSWER 7 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3
SO EMBO Reports (2002), 3(10), 951-955
CODEN: ERMEAX; ISSN: 1469-221X

=> d 9 ab

L21 ANSWER 9 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN
AB The present invention relates to DNA which encodes proteins involved in
gene **silencing**. Related genes encoding proteins characterized
by an amino acid sequence comprising a component sequence of at least 150
amino acid residues having 40% or more identity with an aligned component
sequence of SEQ ID NO:3 can be isolated from different sources such as
mammalian or **plant** cells. Further disclosed is a method for
isolating DNA according to the invention.

=> d 9 pi

L21 ANSWER 9 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001000801	A2	20010104	WO 2000-EP5761	20000621
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1185657	A2	20020313	EP 2000-945801	20000621
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,			

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=> d 10 so

L21 ANSWER 10 OF 19 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN

SO Current Opinion in Genetics and Development, (April, 2001) Vol. 11, No. 2,
pp. 215-220. print.
ISSN: 0959-437X.

=> d 11-19 ti

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(2004) on STN DUPLICATE 4

TI Gene **silencing** and DNA methylation processes.

L21 ANSWER 12 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5

TI Endogenous targets of **transcriptional gene silencing**
in arabidopsis

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(2004) on STN DUPLICATE 6

TI **Transcriptional gene silencing** mutants.

L21 ANSWER 14 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 7

TI Disruption of the **plant** gene MOM releases
transcriptional silencing of methylated genes

L21 ANSWER 15 OF 19 AGRICOLA Compiled and distributed by the National
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of America. It contains copyrighted materials. All rights reserved.
(2004) on STN

TI Disruption of the **plant** gene MOM releases
transcriptional silencing of methylated genes.

L21 ANSWER 16 OF 19 CAPLUS COPYRIGHT 2004 ACS on STN

TI Release of epigenetic gene **silencing** by trans-acting mutations
in Arabidopsis

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(2004) on STN DUPLICATE 8

TI Cytosine methylation at CG and CNG sites is not a prerequisite for the
initiation of **transcriptional gene silencing** in
plants but it is required for its maintenance.

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of America. It contains copyrighted materials. All rights reserved.
(2004) on STN DUPLICATE 9

- TI Methylation of cytosines in nonconventional methylation acceptor sites can contribute to reduced gene expression.
- L21 ANSWER 19 OF 19 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
- TI Two means of **transcriptional** reactivation within heterochromatin.